

FIG. 1A

1 TTTCTCTACTGACTATAAAGAATAGAGAAGGAAGGGCTTCAGTGACCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGATC  
 91 ATGGCTATGATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCTCTGCACTCTCTGTG  
 1 MetAlaMetMetGluValGlnGlyGlyProSerLeuGlyGlnThrCysValLeuIleValIlePheThrValLeuLeuGlnSerLeuCys  
 181 GTGGCTGTAACCTTACGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTCTTAAAGAA  
 31 ValAlaValThrTyrValTyrPheThrAsnGluLeuLysGlnMetGlnAspLysTyrSerLysSerGlyIleAlaCysPheLeuLysGlu  
 271 GATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAG  
 61 AspAspSerTyrTrpAspProAsnAspGluGluSerMetAsnSerProCysTrpGlnValLysTrpGlnLeuArgGlnLeuValArgLys  
 361 ATGATTTTGAGAACCTCTGAGGAAACCATTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCTAGTGAGAGAAAGAGGTCTCTCAG  
 91 MetIleLeuArgThrSerGluGluThrIleSerThrValGlnGluLysGlnGlnAsnIleSerProLeuValArgGluArgGlyProGln  
 451 AGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAA  
 121 ArgValAlaAlaHisIleThrGlyThrArgGlyArgSerAsnThrLeuSerSerProAsnSerLysAsnGluLysAlaLeuGlyArgLys  
 541 ATAAACTCCTGGGAATCATCAAGGAGTGGGCATTTCCTGAGCAACTTGCACTTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGG  
 151 IleAsnSerTrpGluSerArgSerGlyHisSerPheLeuSerAsnLeuHisLeuArgAsnGlyGluLeuValIleHisGluLysLys  
 631 TTTTACTACATCTATTTCCCAACATACTTTTCGATTTTCAGGAGGAAATAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATT  
 181 PheTyrTyrIleTyrSerGlnThrTyrPheArgPheGlnGluGluIleLysGluAsnThrLysAsnAspLysGlnMetValGlnTyrIle  
 721 TACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTAT  
 211 TyrLysTyrThrSerTyrProAspProIleLeuLeuMetLysSerAlaArgAsnSerCysTrpSerLysAspAlaGluTyrGlyLeuTyr  
 811 TCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTGTGTTCTGTAACAAATGAGCACTTGATAGACATGGACCAT  
 241 SerIleTyrGlnGlyGlyIlePheGluLeuLysGluAsnAspArgIlePheValSerValThrAsnGluHisLeuIleAspMetAspHis  
 901 GAAGCCAGTTTTTTTCGGGGCCTTTTTAGTTGGCTAACTGACCTGGAAAGAAAAGCAATAACCTCAAAGTGACTATTTCAGTTTTTCAGGAT  
 271 GluAlaSerPhePheGlyAlaPheLeuValGlyStp  
 991 GATACACTATGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAA

FIG. 1B

41BBL 80 DPAGLLDLRQGMFAQLVAQ-----NVLLIDGPEL-----SMYSDPGLAGVSLTG-GLSYKEDTKELVVA  
 OX40L 52 VSH---RYPRIQSIKVQFT-----EYKKEKG-----F--ILTS---QKED-IMKVQNN--SVIIN  
 CD27L 45 QQQLPLESLGWDVAELQLN-----HTGPEQDPRLEL-----YWGQGPALGRSFLH--GPELDKGL--QLRIH  
 CD30L 87 LCILKRAPPFKSWAYLQVA-----KHLNKTKL-----SWNKD-----GILH--GVRYQDG--NLVIQ  
 TNF 77 VRSSSRTPSDKPVAAHVAN-----PQAEQQL-----QWLNRRAN--ALLAN--GVELRDN--QLVVP  
 LTb 77 EEPETDLSPGLPAHLIGA-----PLKGQGL-----GWETTKEQ--AFLTS--GTQFSDA--EGLALP  
 LTa 52 PKMHLAHTLKPAAHLIGD-----PSKQNSL-----LWRANTDR--AFLQD--GFSLSNN--SLLVIP  
 CD40L 113 MQ--KGDQNPQIAAHVISE-----ASSKTTSVL-----QWAEKGY--TMSNN--LVTLENG--KQLTVK  
 Apo1L 134 PSPPPPEKKELRKVAHLTGK-----SNSRSMPL-----EWEDTYGIV-VLLS--GVKYKKG--GLVIN  
 Apo2L 114 VRE---RGPQRVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH-SFLS--NLHLRNG--ELVIH  
 41BBL 137 KAGVYYVFFQLELRRVAGEGS-----GSVSLALHLQPLRSAAGAAALATVDLPPAS-----  
 OX40L 97 CDGFYLLISLKGVE-SQE-----VNISLH-VQKDE--EP-LFQLKKVRSVN-----  
 CD27L 100 RDGIYMVHIOVTLAICSSTTASRH--HPTTLAVGICSPAS--RSISLLRLSFH-----  
 CD30L 135 FPGLYFIICQLQFLVQCP-----NNSVDLKLLELLINKHI--KKQALVTVCES-----  
 TNF 128 SEGGLYLIYSQVLFKGGGCP-----STHVLLTHTISRIAVSY-QTKVNLLSAIKSPCQRETPE--  
 LTb 129 QDGLYYLYCLVGYRGAPPGGGDPQGRSVTLRSSLYRAGGAYGPGTPELLLEGAETVTPVLDPARR  
 LTa 103 TSGIYFVYSQVVFSGKAYS PKAT--SSPLYLAHEVQLFSQY--PFHVPLLSQKMVYPGL-----  
 CD40L 165 RQGLYYIYAQVTFCSNREA-----SSQAPFIASLCLKSPGR--FERILLRAANTHSSAK-----  
 Apo1L 186 ETGLYFVYSKVYFRGQSC-----NNLPESHKVYMRNSKY--PQDLVMMEGKMMSYCTT-----  
 Apo2L 178 EKGFIYIYSQTYFRFQEEIKENTK--NDKQMVQYIYKYTS--Y-PDPILLMKSARNSCWSKDA----  
 41BBL 190 ----SEARNSAFGFQGRLLHLS-AGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPEIPAGLPSRSE  
 OX40L 137 ----SLMVASLTYKDK----VYLVNVTDTNT-SLDDFHVNGGELILIHQNPGEFCVL  
 CD27L 149 ----FHQGTIVSQRLTPLAR--GDTLCTNLGTGL-LPSRNTD-----ETFGVQWVRP  
 CD30L 180 --GMQTKHVYQNLSQLLDYLVQVNTTISVNVDTFQYI-DTSTFPLEN--VLSIFLYSNSD  
 TNF 184 GAEAKPWEPIYVGGVLEK--GDRLSAEINRPDY--DFAESG-----QVYFGIIAL  
 LTb 195 QGYGPLWYTSVGFGLVQLRR--GERVYVNI SHPDY--DFARG-----KTFEGAVMVG  
 LTa 160 --QEPWLHSMYHGAAPQLTQ--GDQLSTHTDGIPHLLVLSPT-----VVEFGAFAL  
 CD40L 217 ----PCGQSIHLGGVFELOP--GASVFVNVTDPSQVSHGTG-----FTSFGLLKL  
 Apo1L 237 --GQMWARSYLVGAVFNLT--ADHLVYVNVSEL-SLVNFEEES-----QTFEGLYKL  
 Apo2L 236 --EYGLY-SIYQGGIFELKE--NDRIFFSVTNE-HLIDMDHE-----ASFEGAFVLG

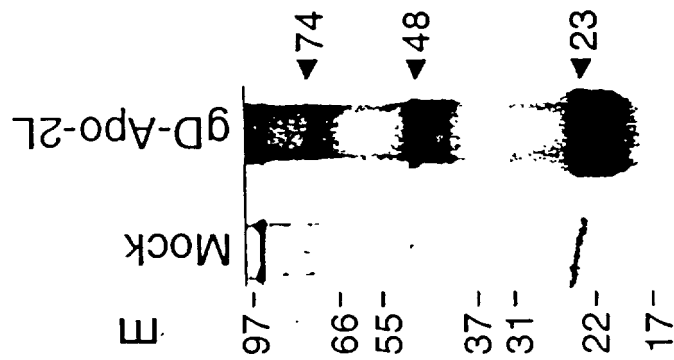


FIG. 1E

FIG. 1D



FIG. 1C

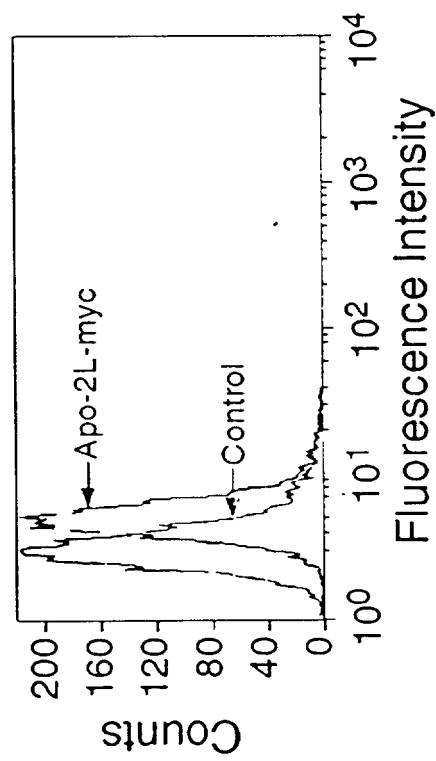


FIG. 2A 9D cells

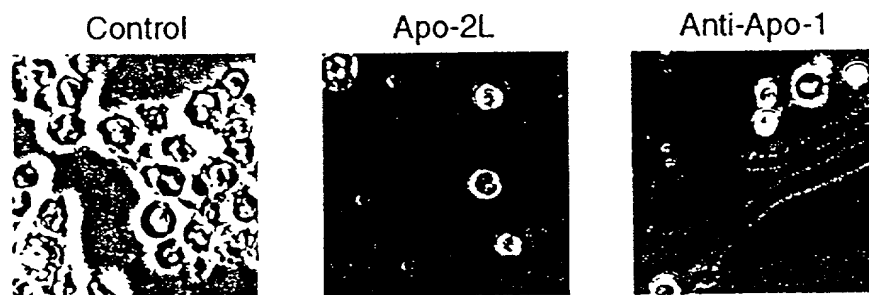


FIG. 2B 9D cells

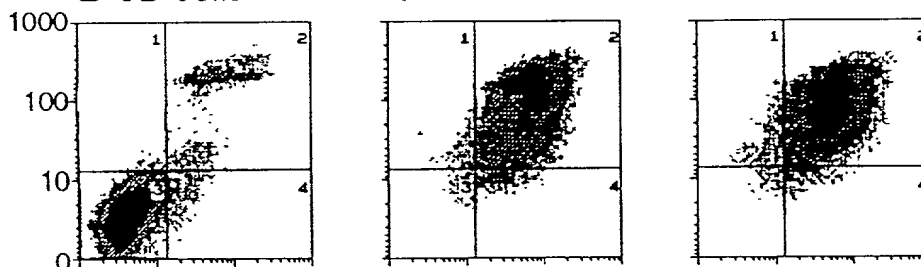


FIG. 2C Raji cells

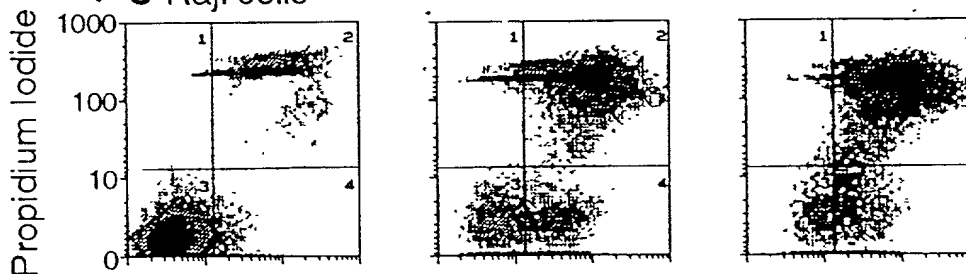


FIG. 2D Jurkat cells

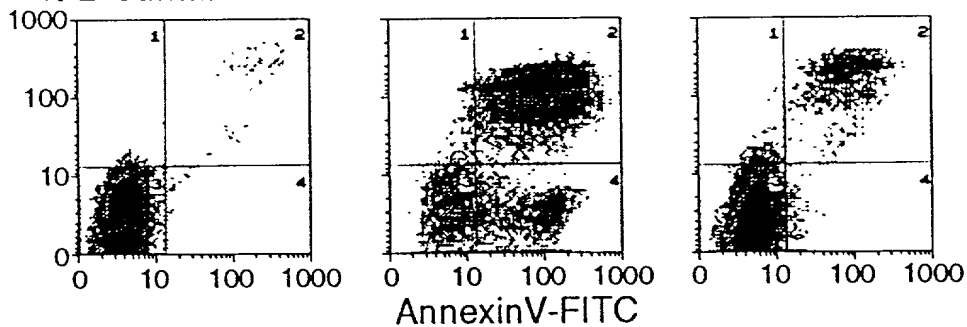


FIG. 2E



FIG. 3 A

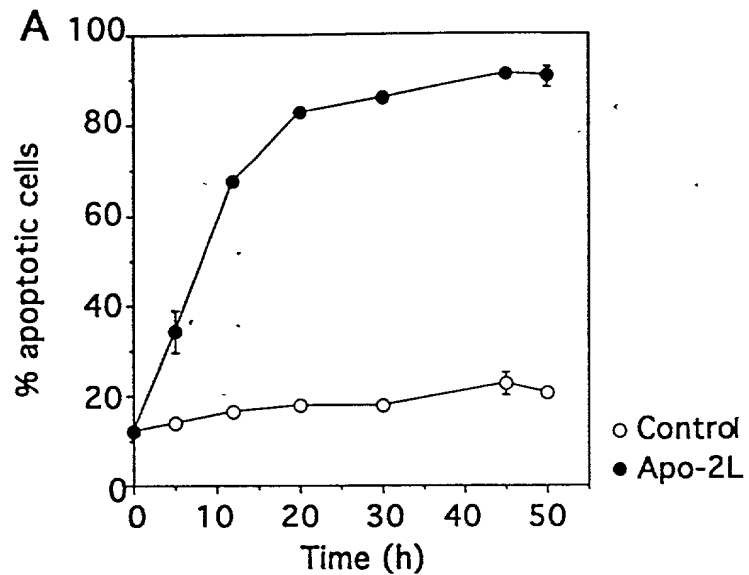


FIG. 3 B

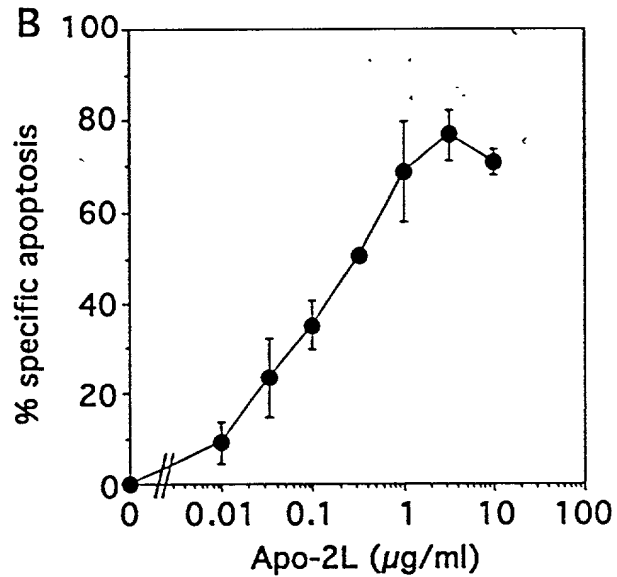


FIG. 3 C

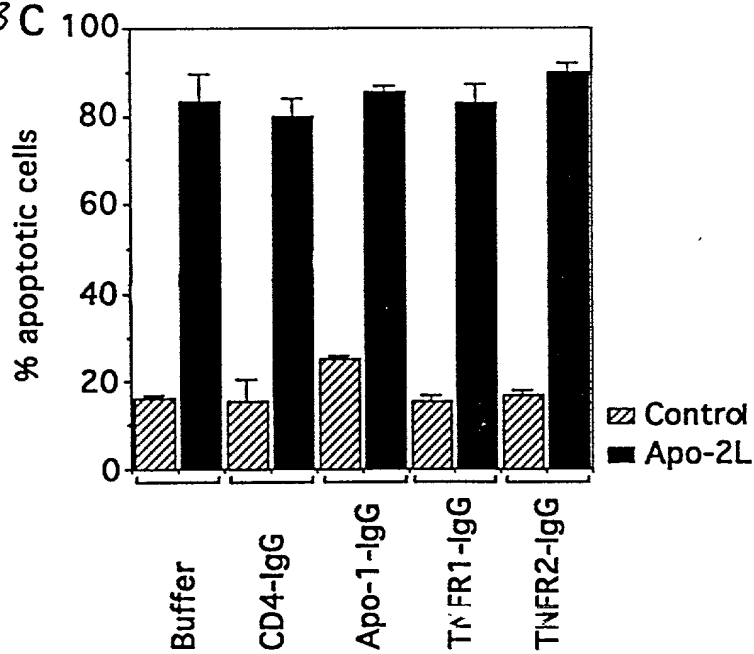


FIG. 4

